SAIC-Frederick
An Employee-Owned Company
A Subsidiary of SAIC

To: Robert M. Stephens, Ph.D., Director, Bioinformatics Support Group
Advanced Biomedical Computing Center, ISP, ATP, SAIC-Frederick, Inc.

From: Laura S. Schmidt, Ph.D., Principal Scientist, Basic Science Program
SAIC- Frederick, Inc. and Urologic Oncology Branch, NCI

Date: May 5, 2010

RE: Letter of Support for work performed by the Bioinformatics Support Group, Advanced Biomedical Computing Center (ABCC)

It is with great pleasure that I am writing this letter to acknowledge the outstanding scientific computing work performed by the Bioinformatics Support Group at the ABCC in support of the Urologic Oncology Branch, NCI. I have been working with Dr. Natalia Volfovsky on two projects over the past 5 months.

The first collaborative project involves analysis of data generated from eight GS Titanium FLX 454 sequencing runs. Dr. Volfovsky has combined data from two sequencing facilities, performed a quality check, analyzed the data using in-house software, and generated well organized, user-friendly excel files, in which single nucleotide sequence variants that were filtered to remove common variants, have been organized and subclassified into those which affect the protein and appear in at least 2 of 4 samples. These files also contain important information regarding sequence coverage of regions within the genome, number of samples in which the variant was detected, and coordinates to identify chromosomal location in order to enable our assessment of the quality of the data. She has produced many other files available on the server detailing in/dels and large sequence variations that I look forward to analyzing when converted to a more user-friendly format.

During my interactions with Dr. Volfovsky, I have been impressed with her professionalism, high level of knowledge of and expertise in her field, and broad understanding of the next generation sequencing technology and experimental approaches. She provided me with articles to read and asked me very specific questions regarding how I would like the data analyzed, then responded by addressing those scientific questions in a comprehensive and detailed manner. Prior to actually beginning the 454 sequencing project, I met with Dr. Volfovsky and Dr. Bob Stephens to discuss the overview of the entire project, the approaches that would be taken for data analysis, and time frame for the work. Since I was new to this type of research, I found the explanations of the approaches they would recommend and method of data analysis provided by the BSG team to be very informative and educational for me, and I gained a great deal from our meeting as they patiently answered my many questions.

The second collaborative project involves analysis of micro RNA sequencing data generated from 16 normal and tumor mouse and human samples produced by the Sequencing Facility Core at the NCI. Currently Dr. Volfovsky has not received all of the data so the project is in its early stages. However, we have received good communication from her updating us on the status of the project with some preliminary data to indicate the quality of the sequencing runs and numbers of miRNAs per sample. She very astutely identified a discrepancy in the data early on, that facilitated some necessary resequencing. Again she has demonstrated a strong knowledge base regarding miRNA regulation and provided me with literature references that I found very useful.

As mentioned both of these projects are ongoing and I am looking forward to continued fruitful collaborations and exciting gene discoveries from these data. I have been extremely satisfied in my collaborations with Drs. Volfovsky and Stephens and therefore strongly recommend the Bioinformatics Support Group to the NCI research community at large for computing needs in their research.

Laura S Schmidt

Laura S. Schmidt, PhD
Principal Scientist
BSP, SAIC-Frederick, Inc.
NCI-Frederick and
Urologic Oncology Branch
National Cancer Institute, NIH